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May 1, 2003

Ms. Shirley Steele
U.S. Patent and Trademark Office
2011 South Clark Place
Crystal Plaza 2, Room 7D25
Arlington, VA 22202

Re: US Patent Application No. 09/870,353
For: IMPROVED NUCLEIC ACID MODIFYING ENZYMES
Inventors: Yan Wang, et al.
Filed: May 30, 2001
Our File No.: 020130-000111US

Dear Ms. Steele:

The enclosed replacement sequence listing diskette with paper copy and statement letter is being sent to you pursuant to our telephone conversation today. Please let me know if you need anything else. Thank you for your assistance.

Very truly yours,

Jean M. Lockyer, Ph.D.
Patent Agent

JML/mcd
Enclosure

SF 1456680 v1



I hereby certify that this is being send via "FedEx" on May 1, 2003

to:

Ms Shirley Steele
U.S. Patent and Trademark Office
2011 South Clark Place
Crystal Plaza 2, Room 7D25
Arlington, VA 22202

TOWNSEND and TOWNSEND and CREW LLP

By: Malinda A. Wolf

PATENT
Attorney Docket No.: 020130-000111US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

WANG *et al.*

Application No.: 09/870,353

Filed: May 30, 2001

For: IMPROVED NUCLEIC ACID
MODIFYING ENZYMES

Examiner: Not yet assigned

Art Unit: 1633

SUBMISSION OF REPLACEMENT COPY
OF SEQUENCE LISTING

Ms Shirley Steele
U.S. Patent and Trademark Office
2011 South Clark Place
Crystal Plaza 2, Room 7D25
Arlington, VA 22202

Sir:

In response to the May 1, 2003 telephone request for a replacement copy of the computer readable form (CRF) of the Sequence Listing that was previously filed on August 5, 2002, Applicants submit herewith the requested replacement CFR and paper copy of the Sequence Listing.

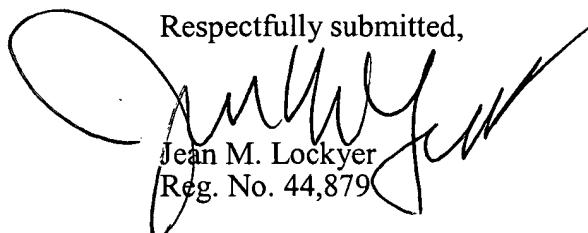
The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

WANG *et al.*
Application No.: 09/870,353
Page 2

PATENT

If it is believed that a telephone conference would expedite prosecution of
this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,


Jean M. Lockyer
Reg. No. 44,879

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JML:dmw
SF 1456614 v1



#12

SEQUENCE LISTING

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Xi, Lei
Prosen, Dennis E.
MJ Bioworks, Inc.

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 aagttctgca aggacatccc tggtttata ccaagtctct tggacattt gttagaggaa 1380
 agacaaaaga ttaagacaaa aatgaagggaa actcaagatc ctatagaaaa aataactcctt 1440
 gactatagac aaaaagcgat aaaactctt gcaatttctt tctacggata ttatggctat 1500
 gcaaaaagcaa gatggtaactg taaggaggtt gctgagagcg ttactgcctg gggaaagaaaag 1560
 tacatcgagt tagtattggaa ggagctcgaa gaaaagttt gattttaaagt cctctacatt 1620
 gacactgatg gtctctatgc aactatccca ggaggagaaa gtgaggaaat aaagaaaaag 1680
 gctctagaat ttgtaaaata cataaattca aagctccctg gactgctaga gcttgaatatt 1740
 gaagggtttt ataagagggg attcttcgtt acgaagaaga ggtatgcagt aatagatgaa 1800
 gaaggaaaag tcattactcg tggtttagag atagtttaga gagattggag taaaattgca 1860
 aaagaaaactc aagcttagagt tttggagaca atactaaaac acggagatgt tgaagaagct 1920
 gtgagaatag taaaagaagt aatacaaaaag cttgccaattt atgaaattcc accagagaag 1980
 ctcgcaatat atgagcagat aacaagacca ttacatgagt ataaggcgat aggtcctcac 2040
 gtagctgtt caaagaaaact agctgctaaa ggagttaaaa taaagccagg aatggtaatt 2100
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 ggtgcaaccg taaagttcaa gtacaaaggc gaagaaaaag agtagacat ctccaagatc 2400
 aagaaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cggtgccaaag 2460
 accggccgtg gtgcggtaag cgaaaaggac gcggcgaagg agctgctgca gatgctggag 2520
 aagcagaaaaa agtga 2535

<210> 8
 <211> 844
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 Pfu-Ssod7d

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 Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
 20 25 30
 Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
 35 40 45
 Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
 65 70 75 80
 Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
 355 360 365
 Pro Asn Lys Pro Ser Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
 385 390 395 400
 Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
 420 425 430
 Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Glu Ser Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
 595 600 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
 625 630 635 640
 Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
 835 840

<210> 9
 <211> 1904
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:fusion protein
 Sac7d-deltaTaq

 <220>
 <221> CDS
 <222> (1)..(1904)
 <223> Sac7d-deltaTaq

<400> 9
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 gacacttcaa agataaaagaa gtttggaga gttagcaaaa tggtgtcctt tacctatgac 120
 gacaatggta agacaggtag aggagctgt a c g a g a a a g a t g c t c c a a a g a a t t a t t a 180
 gacatgttag caagagcaga a a g a g a a a g g g c g g c g t g t c a c t a g t c c c a a g g c c 240
 ctggaggagg ccccttggcc cccgcccggaa gggccttcg tggctttgt gctttcccg 300
 aaggagccca t g t g g g c c g a t c t t c t g g c c c t g g c c c g c c a g g g g g g g g c c 360
 cggggccccc a g c c t t a t a a a g c c t c a a g g a c t g a a g g a g g c g g g g g g g c t c t c g c c 420
 a a a g a c c t g a g c t t c t g g c c t g a g g g g a a g c t t g g c c t c c c c g a c g a c c c c 480
 a t g c t c t c g c c t a c c t c c t g a g g g g g g a c a c c a c c c c c g a g g g g g g t g g c c g g c g c 540
 t a c g g c g g g g a g t g g a c g g a g g g c g g g g g g a c c a c c c c c c t t c c g a g g g c t t c 600
 g c c a a c c t g t g g g g a g g g g g g t g a g g g g g g a g g g c t c c g g g g a g g t g 660
 g a g a g g c c c c t t c c t g g c c a c a t g g a g g c c a g g g g g g t g c c t g g a c g t g 720
 g c c t a t c t a g g c c t t g t c c t g g a g g t g g c c g a g g g a a t c g c c c c t c c g a g g c c g g g 780
 t c t t c c g c c t g g c c a c c t c a a c t c c c g g a c a g g t g g a a a g g g t c c 840

tctttacgca gctagggttt cccggccatcg gcaagacgga gaagaccggc aagcgctcca 900
 ccagcgccgc cgtctggag gcccctccgcg agggccaccc cattcggtggag aagatcctgc 960
 agtaccggga gctcaccacaa ctgaagagca cttacattga ccccttgcgc gacctcatcc 1020
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 taagtagctc cgatcccaac ctccagaaca tccccgtccg caccggcgtt gggcagagga 1140
 tccggccgggc cttcatcgcc gaggagggtt ggctattgtt ggccttggac tatagccaga 1200
 tagagctcag ggtgtggcc cacctctccg ggcacggaaa cctgatccgg gtcttccagg 1260
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 gcaggaggcg ggggtacgtg gagaccctt tcggccgcgc cgcgtacgtg ccagacctag 1560
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 agggcaccgc cggcggacccatc atgaagctgg ctatggtggaa gctttttttt aggctggagg 1680
 aaatgggggc caggatgttc cttcagggtcc acgacgagct ggtcctcgag gccccaaaag 1740
 agagggcgggaa gggcgtggcc cggctggcca aggaggtcat ggaggggggtt tatccccctgg 1800
 ccgtccccctt ggagggtggag gtggggatag gggaggactg gctctccgccc aaggagggca 1860
 ttatggccggc cggcggagggc gggcatcatc atcatcatca tttaa 1904

<210> 10
 <211> 634
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 Sac7d-deltaTaq

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 1 5 10 15
 Glu Lys Glu Val Asp Thr Ser Lys Ile Lys Lys Val Trp Arg Val Gly
 20 25 30
 Lys Met Val Ser Phe Thr Tyr Asp Asp Asn Gly Lys Thr Gly Arg Gly
 35 40 45
 Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Asp Met Leu Ala
 50 55 60
 Arg Ala Glu Arg Glu Lys Lys Gly Gly Val Thr Ser Pro Lys Ala
 65 70 75 80
 Leu Glu Glu Ala Pro Trp Pro Pro Glu Gly Ala Phe Val Gly Phe
 85 90 95
 Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala
 100 105 110
 Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
 115 120 125
 Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
 130 135 140
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
 145 150 155 160
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 165 170 175
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
 180 185 190
 Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
 195 200 205
 Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
 210 215 220
 Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
 225 230 235 240

Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
 245 250 255
 Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 260 265 270
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
 275 280 285
 Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 290 295 300
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 305 310 315 320
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
 325 330 335
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 340 345 350
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 355 360 365
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 370 375 380
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 385 390 395 400
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 405 410 415
 Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp
 420 425 430
 Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 435 440 445
 Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 450 455 460
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
 465 470 475 480
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 485 490 495
 Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
 500 505 510
 Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
 515 520 525
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 530 535 540
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
 545 550 555 560
 Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu
 565 570 575
 Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
 580 585 590
 Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
 595 600 605
 Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly Ile Asp Gly Arg
 610 615 620
 Gly Gly Gly His His His His His His
 625 630

<210> 11
 <211> 1965
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 PL-deltaTaq

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<220>
<221> CDS
<222> (1)..(1965)
<223> PL-deltaTaq

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gaggtagaca tctccaagat caagaaagta tggcggtgtgg gcaagatgtat ctccttcacc 180
tacgacgagg gcggtggcaa gaccggccgt ggtgcggtaa gcgaaaagga cgccgccaag 240
gagctgtgc agatgtcgaa gaagcagaaa aaggcgccg gtgtcaccag tcccaaggcc 300
ctggaggagg cccctggcc cccgcccggaa ggggccttcg tggcgtttgt gctttccgc 360
aaggagccca tggggccga tcttctggcc ctggccgccc ccaggggggg cccgggtccac 420
cgggcccccg agccttataa agccctcagg gactgtaaagg aggccgggg gcttctcgcc 480
aaagacctga gcgttctggc cctgaggaa ggccttggcc tcccgcccg cgacgacc 540
atgctctcg cctaccttcg ggacccttc aacaccaccc ccgagggggtt gggccggcgc 600
tacggcgggg agtggacgga ggaggcgaaa gaggccgccc cccttccga gaggcttcc 660
gccaacctgt gggggagggt tgaggggggag gagaggctcc tttggctta cccgggagggt 720
gagaggcccc tttccgtgt cctggcccac atggaggcca cgggggtgcg cctggacgtg 780
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ctcttgcac agcttagggct tcccgcaccc gcaagacgg agaagaccgg caagcgctcc 960
accagcgccg ccgttctggc ggccttcgc gaggcccacc ccatgttggaa gaagatcctg 1020
cagtaccggg agctcaccaa gctgaagagc acctacattt accccttgcg ggaccttcattc 1080
ccccccagga cggggccct ccacaccgc ttcaaccaga cggccacccgc cacgggcagg 1140
ctaagtagct ccgttccaa cctccagaac atccccgtcc gcaccccgct tggcagagg 1200
atccgcggg ctttcatcg c gaggagggg tggctattgg tggcccttggaa ctatagccag 1260
atagagctca gggtgcgtgc ccaccttc ggcgacgaga acctgtatccg ggtcttccag 1320
gagggggcgaa acatccacac ggagaccgc agctggatgt tcggcgtccc cccgggaggcc 1380
gtggacccccc tgatgcggc ggcggccaa accatcaact tcggggctt ctacggcatg 1440
tcggccacc gcctctccca ggagctagcc atcccttacg aggaggccca ggccttcatt 1500
gagcgctact ttcagagctt ccccaaggtg cggccttggaa ttgagaagac cctggaggag 1560
ggcaggaggc ggggtacgt ggagaccctc ttccggccgccc gccgctacgt gccagaccta 1620
gaggcccgaa tgaagagcgt gcgaggcg gcccggcga tggccttcaa catgcccgtc 1680
caggccaccg cgcggccaccc catgaagctg gctatggtga agcttccc caggctggag 1740
gaaatggggg ccaggatgtt ctttcaggtt caccacgagc tggccttgcg gggcccaaaa 1800
gagagggcgaa aggccgtggc ccggcttggcc aaggaggta tggaggggggt tataccctg 1860
ggcggtcccc tggaggttggaa ggtggggata gggaggact ggcttccgc caaggaggc 1920
attgtatggcc gcggcggagg cggccatcat catcatcatc attaa 1965

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<210> 12
<211> 654
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:fusion protein
      PL-deltaTaq

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<400> 12
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Lys Lys Lys Lys Lys Gly Gly Val Thr Ser Gly Ala Thr Val Lys
  20          25          30
Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
  35          40          45
Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
  50          55          60
Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
  65          70          75          80

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Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Gly Gly Gly Val Thr
 85 90 95
 Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
 100 105 110
 Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu
 115 120 125
 Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu
 130 135 140
 Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala
 145 150 155 160
 Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro
 165 170 175
 Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
 180 185 190
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu
 195 200 205
 Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp
 210 215 220
 Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val
 225 230 235 240
 Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val
 245 250 255
 Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu
 260 265 270
 Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro
 275 280 285
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 290 295 300
 Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser
 305 310 315 320
 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 325 330 335
 Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr
 340 345 350
 Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His
 355 360 365
 Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
 370 375 380
 Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
 385 390 395 400
 Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu
 405 410 415
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 420 425 430
 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu
 435 440 445
 Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu
 450 455 460
 Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
 465 470 475 480
 Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala
 485 490 495
 Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
 500 505 510
 Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu
 515 520 525
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val
 530 535 540
 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
 545 550 555 560

Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
 565 570 575
 Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp
 580 585 590
 Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg
 595 600 605
 Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu
 610 615 620
 Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly
 625 630 635 640
 Ile Asp Gly Arg Gly Gly Gly His His His His His His His
 645 650

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer L71F

<400> 13
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<210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer L71R

<400> 14
 gcacagcggc tggctgagga 20

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer L18015F

<400> 15
 tgacggagga taacgccagc ag 22

<210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer L23474R

<400> 16
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<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L18015F

<400> 17
tgacggagga taacgccagc ag 22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L29930R

<400> 18
gggggttggag gtcaatgggt tc 22

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L30350F

<400> 19
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<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L35121R

<400> 20
cacatggtag agcaaggctg gc 22

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L2089F

<400> 21
cccgtagatctg ctgggatact ggc 23

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<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L7112R

<400> 22
cagcggtgct gactgaatca tgg 23

<210> 23
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L30350F

<400> 23
cctgcctgcc gtttcacgc 19

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L40547R

<400> 24
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<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
      H-Amelo-Y

<400> 25
ccacccatc ctgggcacc 19

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
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<400> 26
gcttgaggcc aaccatcaga gc 22

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<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:human
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<400> 27
ggttggccaa tctactccca gg

<210> 28
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
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<400> 28
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<210> 29
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<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6-His epitope
      tag

<400> 30
His His His His His His
      1           5

<210> 31
<211> 8
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anti-DYKDDDDK
      epitope tag

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22

20

24

<400> 31
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 32
<211> 4
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

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Gly Gly Val Thr
1

<210> 33
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

<400> 33
Gly Thr Gly Gly Gly Gly
1 5

<210> 34
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:lysine-rich peptide

<400> 34
Asn Ser Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg Lys Lys Lys
1 5 10 15
Gly Gly Gly Val Thr
20